Guiding questions :

- What are gene-gene interactions? What is the difference between biological and statistical epistasis?
- Is it hard to detect epistasis? Which factors make it harder to perform a genome-wide association interaction study as compared to a genome-wide main effects association study?
- What does it take to increase your chances to detect gene-gene interactions? (in terms of design? methods? subject sample size? marker sample size?)
- What have gene-environment and gene-gene interaction screening in common / not in common? Do they need to be analyzed differently? Why? Why not?
- What is environmental epigenetics? Is this an example of gene-environment interaction? Are there other forms of epigenetics?

Specifically related to the trait chosen in your homework 1:

- Has evidence been found for genetic factors modifying the effect of identified genes for the chosen trait? Describe which evidence and how this evidence was derived/obtained.
- Has evidence been found for non-genetic factors modifying the effect of identified genes for the chosen trait?
  Describe which evidence and how this evidence was derived/obtained.
- Has knowledge about gene-gene and/or gene-environment interactions already impacted disease treatment or public health policies? Give examples.
- Is the evidence for your chosen trait, that identified genetic causal markers affect the expression or translation of other (more distant) genes? If so, describe. Is this also a form of gene-gene interaction? Link back to the definitions you can find about gene-gene interactions.

Group 1 : melanoma

http://www.genomel.org/

Group 2 : phenylcétonurie

see documentation posted on the course website

Group 3: breast cancer

http://ccge.medschl.cam.ac.uk/consortia/bcac/

Group 4: Crohn's disease

IIBDGC = international ibd genetics consortium